

50	55	60
Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys 65 70 75 80		
Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu 85 90 95		
His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val 100 105 110		
Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val 115 120 125		
His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu 130 135 140		
Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu 145 150 155 160		
Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp 165 170 175		
Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln 180 185 190		
Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu 195 200 205		
Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly 210 215 220		
Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr 225 230 235 240		
Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met 245 250 255		
Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys 260 265 270		
Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro 275 280 285		
Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu 290 295 300		

<210> 3

<211> 915

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(915)

<220>

<223> Description of Artificial Sequence:pkc chimera

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Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe

48

1	5							10					15					
gtc cga act ggc tat ggg aag gat atg ata aaa gtt ctc cat att cag	Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln	96																
20 25 30																		
cga gat gga aaa tat cac agc att aaa gag gtg gca act tca gtg caa	Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln	144																
35 40 45																		
ctg act ttg agc tcc aaa aaa gat tac ctg cat gga gac aat tca gat	Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp	192																
50 55 60																		
gtc atc cct aca gac acc atc aag aac aca gtt aat gtc ctg gcg aag	Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys	240																
65 70 75 80																		
ttc aaa ggc atc aaa agc ata gaa act ttt gct gtg act atc tgt gag	Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu	288																
85 90 95																		
cat ttc ctt tct tcc ttc aag cat gtc atc aga gct caa gtc tat gtg	His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val	336																
100 105 110																		
gaa gaa gtt cct tgg aag cgt ttt gaa aag aat gga gtt aag cat gtc	Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val	384																
115 120 125																		
cat gca ttt att tat act cct act gga acg cac ttc tgt gag gtt gaa	His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu	432																
130 135 140																		
cag ata agg aat gga cct cca gtc att cat tct gga atc aaa gac cta	Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu	480																
145 150 155 160																		
aaa gtc ttg aaa aca acc cag tct ggc ttt gaa gga ttc atc aag gac	Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp	528																
165 170 175																		
cag ttc acc acc ctc cct gag gtg aag gac cgg tgc ttt gcc acc caa	Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln	576																
180 185 190																		
gtg tac tgc aaa tgg cgc tac cac cag ggc aga gat gtg gac ttt gag	Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu	624																
195 200 205																		
gcc acc tgg gac act gtt agg agc att gtc ctg cag aaa ttt gct ggg	Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly	672																
210 215 220																		
ccc tat gac aaa ggc gag tac tcg ccc tct gtc cag aag aca ctc tat	Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr	720																
225 230 235 240																		
gac atc cag gtg ctc acc ctg ggc cag gtt cct gag ata gaa gat atg	Asp Ile Gln Val Leu Thr Leu Gly Gln Val Pro Glu Ile Glu Asp Met	768																
245 250 255																		
gaa atc agc ctg cca aat att cac tac tta aac ata gac atg tcc aaa		816																

Glu Ile Ser Leu Pro Asn Ile His Tyr Leu Asn Ile Asp Met Ser Lys
 260 265 270

atg gga ctg atc aac aag gaa gag gtc ttg cta cct tta gac aat cca 864
 Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro
 275 280 285

tat gga aaa att act ggt aca gtc aag agg aag ttg tct tca aga ctg 912
 Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu
 290 295 300

tga 915

305

<210> 4

<211> 304

<212> PRT

<213> Artificial Sequence

<400> 4

Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe
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Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln
 20 25 30

Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln
 35 40 45

Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp
 50 55 60

Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys
 65 70 75 80

Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu
 85 90 95

His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val
 100 105 110

Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val
 115 120 125

His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu
 130 135 140

Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu
 145 150 155 160

Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp
 165 170 175

Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln
 180 185 190

Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu
 195 200 205

Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly
 210 215 220